

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Docket No.: 1/1144  
Application of: Jung, Birgit et al ) Art Unit: To be assigned  
Serial No. : To be assigned ) Examiner: To be assigned  
Filed : August 31, 2001  
For : Method for identifying substances which positively influence  
inflammatory conditions of chronic inflammatory airway disease

Assistant Commissioner for Patents  
Washington, D.C. 20231

STATEMENT BY ATTORNEY UNDER 37 C.F.R. § 1.821(f)  
REGARDING SEQUENCE LISTING

Sir:

Attorney for Applicants affirms that the information recorded in computer readable form is identical to the written sequence listing.

Respectfully submitted,

*Susan K. Pocchiari*

Susan K. Pocchiari  
Attorney for Applicant(s)  
Reg. No. 45,016

Patent Department  
Boehringer Ingelheim Corp.  
900 Ridgebury Road  
P.O. Box 368  
Ridgefield, CT. 06877  
Tel.: (203) 798-5648

I hereby certify that this correspondence is being deposited with the U.S. Postal Service as express mail (Label No. EL636296388US) in an envelope addressed to:

Assistant Commissioner for Patents  
Washington, DC 20231

on August 31, 2001

*Susan K. Pocchiari*

By: Susan K. Pocchiari  
Reg. No. 45,016

# SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively influence inflammatory conditions of chronic inflammatory airway diseases

<130> 082\_00n

<140>

<141>

<150> UK 0021484.1

<151> 2000-09-01

<160> 24

<170> Patentin Ver. 2.1

<210> 1

<211> 1910

<212> DNA

<213> Homo sapiens

<400> 1

```

gaaaaggagc ttagctgctg gtgctgctgg caagatggaa accaactctc ccaactcctc 60
gaatgaatat gaagaagtgt cctatgagtc tgcctggctac actgtttctg ggatctctcc 120
atttgttggtg cttgggggtca cctttgtcct cgggggtcctg ggcaatgggc ttgtgatctg 180
ggctggctgga ttccggatga cagcacagc caccaccatc tgttacctga aactggccct 240
ggctgacttt tttttcacgg ccacattacc attcctcatt gtctccatgg ccatgggaga 300
aaaatggcct tttggctggg tctgtgttaa gttaattcac atcggtgtgg acatcaacct 360
ctttgggaag gtctctctga ttgggttcat tgcactggac cgctgcattt gtgtcctgca 420
tccagtctgg gccccagaacc accgcactgt gactctggcc atgaagtgta tcgtcggaac 480
ttggattctt gctctagtc ttaccttgcc agttttctc tttttgacta cagtaactat 540
tccaaatggg gacacatact gtactttcaa ctttgcaccc tgggggtggca ccctgagga 600
gaggctgaag gtggccatta ccatgctgac agccagaggg attatccggg ttgtcattgg 660
ctttagcttg ccgagtcca ttgttgccat ctgctatggg ctacttcgag ccaagatcca 720
caaaaaggcg atgattaaat ccagccgtcc cttacggggt ctactctgct tgggtggctt 780
ttttctcatt ttgttggttc cttttcaact ggttgccctt ctggggcacg ctggtgctca 840
agagatgttg ttctatggca agtacaaaat cattgacatc ctggttaaac caccgagctc 900
cctggccttc ttcaacagct gccccaacc catgctttac gtctttgtgg gccaaagact 960
ccgagagaga ctgattccact cctgcccac cagctctggag agggccctgt ctgagagact 1020
agccccaact aatgacacgg ctgccaatc tgcttcacct cctgcagaga ctgagttaca 1080
ggcaatgta ggaatgggtc agggatatt tgagttctgt tcatcctacc ctaatgccag 1140
ttccagcttc atctaccctt gactcatatt gaggcatcca aggatgcaca gctcaagtat 1200
ttatccagga aaaatgcttt ttgtgctcctg atttgggggt aagaaaataga cagtcaaggct 1260
actaaaatat tagtgttatt ttttgttttt tgactctctg ctataccctg gggtaagtgg 1320
agtggggaaa tacaaagaag gaaagaccgg tggggatttg taagacttag atgagatagt 1380
gcataataag ggggaagact taaagtataa agtaaaatgt ttgctgttag ttttttatag 1440
ctattcaaaa aaatcagatt atggaaagttt tcttctattt ttagtgtgct aagagctttt 1500
tgtttctttt tcttcacatc tagctggact ttgcatttta tcaaatgcat ttctacatg 1560
tattaagatg gtcatatatc tcttctcttt ttatgtaaat cattataaat aatgttcat 1620
aagttctctgaa tgttaaaacta ccttgaatt cctggaataa accacactta gtctctgatg 1680
actttaaataa tttatctctc acaggagttg gttagaattt ctgtgtttat gtttatatac 1740
tgtttattca ctttttctac tatccttgct aagttttcat agaaaaaag gaacaaagag 1800
aaacttgtaa tgggtctctga aaaggaattg agaagtaatt cctctgattc tgttttctgg 1860

```

tggtatatct ttattaaata ttcagaaaaa ttcaccagtg aaaaaaaaaa

1910

<210> 2  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Glu Thr Asn Phe Ser Thr Pro Leu Asn Glu Tyr Glu Glu Val Ser  
 1 5 10 15  
 Tyr Glu Ser Ala Gly Tyr Thr Val Leu Arg Ile Leu Pro Leu Val Val  
 20 25 30  
 Leu Gly Val Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile  
 35 40 45  
 Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Thr Thr Ile Cys Tyr  
 50 55 60  
 Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe  
 65 70 75 80  
 Leu Ile Val Ser Met Ala Met Gly Glu Lys Trp Pro Phe Gly Trp Phe  
 85 90 95  
 Leu Cys Lys Leu Ile His Ile Val Val Asp Ile Asn Leu Phe Gly Ser  
 100 105 110  
 Val Phe Leu Ile Gly Phe Ile Ala Leu Asp Arg Cys Ile Cys Val Leu  
 115 120 125  
 His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Met Lys  
 130 135 140  
 Val Ile Val Gly Pro Trp Ile Leu Ala Leu Val Leu Thr Leu Pro Val  
 145 150 155 160  
 Phe Leu Phe Leu Thr Thr Val Thr Ile Pro Asn Gly Asp Thr Tyr Cys  
 165 170 175  
 Thr Phe Asn Phe Ala Ser Trp Gly Gly Thr Pro Glu Glu Arg Leu Lys  
 180 185 190  
 Val Ala Ile Thr Met Leu Thr Ala Arg Gly Ile Ile Arg Phe Val Ile  
 195 200 205  
 Gly Phe Ser Leu Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile  
 210 215 220  
 Ala Ala Lys Ile His Lys Lys Gly Met Ile Lys Ser Ser Arg Pro Leu  
 225 230 235 240  
 Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro  
 245 250 255

Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Leu Lys Glu Met Leu  
260 265 270

Phe Tyr Gly Lys Tyr Lys Ile Ile Asp Ile Leu Val Asn Pro Thr Ser  
275 280 285

Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe  
290 295 300

Val Gly Gln Asp Phe Arg Glu Arg Leu Ile His Ser Leu Pro Thr Ser  
305 310 315 320

Leu Glu Arg Ala Leu Ser Glu Asp Ser Ala Pro Thr Asn Asp Thr Ala  
325 330 335

Ala Asn Ser Ala Ser Pro Pro Ala Glu Thr Glu Leu Gln Ala Met  
340 345 350

<210> 3  
<211> 2433  
<212> DNA  
<213> Homo sapiens

<400> 3  
cagcgcggcg ccatggagccg cgcgcggccg gcccccgccc gcctcggggc gctgctctgc 60  
ctgctgctcg ccgcgtcccg ccgcctggta ggagtgggcg gtgaggagga gctgcagggt 120  
atccagcctg acaagtcctg atcagttgca cctggagagt cggccattct gcactgcact 180  
gtgaactccc tgatccctgt ggggcccatc cagtggttca gaggagctgg accagcccg 240  
gaattaactc acaatcaaaa agaagccac ttcccccg taacaactgt tccagagtcc 300  
acaagagag aaaaatcgga cttttccatc agcatcagta acatcaccac agcagatgcc 360  
ggcacctact actgtgtgaa gttccggaaa gggagccctg acacggagtt taagtctgga 420  
gcaggcactg agctgtctgt cgtgtccaaa cctctgtccc ccgtgtgtatc gggccctgag 480  
gcgagggcca caccctcagca cacagtgcac ttcacctgag agtccccacg cttctcacc 540  
agagacatca ccttgaaatg gttcaaaaat ggggaatgag tctcagactt ccagaccaac 600  
gtggaccccg taggagagag cgtgtcctac agcatccaca gcacagccaa ggtgtgtgct 660  
accgcgaggg acgttccact tcaagtcatc tgcgaggtgg cccacgtcac cttgcagggg 720  
gacctctctc gtgggactgc caactgtctc gagaccatcc gaggttccacc cactctggag 780  
gttactcaac agcccgtgag ggcagagAAC caggtgaatg tcacctgcca ggtgaggaag 840  
ttctaccccc agagactaca gctgacctgg ttggagaagt gaaacgtgtc ccggacagaa 900  
acggctctca cgtctacaga gaacaaggat ggtacctaca actggatgag ctggtctcgt 960  
gtgaatgtat ctgcccacag ggaatgatgt aagctcacct gccaggtgga gcatgacggg 1020  
cagccagcgg tcagcaaaag ccatgacctg aaggtctcag cccaccggaa ggagcaggcg 1080  
tcaaataccg cctgtgagaa cactggatct aatgaacgga acatctatat tbtgtgtggg 1140  
gtggtgtgca cctgtgtgtg ggcctctact atggcgggcc tctacctgtt cgaatcaga 1200  
cagaagaaag cccagggctc cacttctctc acaagggtgc atgagcccca gaagaatgcc 1260  
agagaaatca cacaggacac aaatgataac acatatgcag acctgaacct gcccaagggg 1320  
aagaaagctc ctccccaggc tgggagacc ccaaacacca cggagtatgc cagacttcag 1380  
accagcccg cgcgcgcgtc ggaggacacc ctacactatg ctgacctgga catggtccac 1440  
ctcaacggca ccccgaagca gccggccccc aagcctgagc cgtctctctc agagtacgac 1500  
agcgtccagg tcccagagaa gtgaatggga ccgtggtttg ctctagcacc catctctacg 1560  
cgcttctctg tcccacaggg agccgcctgt atgagcacag ccaaccagat tcccgaggag 1620  
ctggggggctg cagggtctgt ggacccaggg gccagggtgg ctctctctc cccacccctc 1680  
cttgcctctc cagcaactcc tgggcagcca cggcccccct ccccaacatt gccacacac 1740  
tggaggtctga cgttgccaaa ccagccaggg aaccaacctg ggaagtggcc agaactcct 1800  
ggggtccaaag aactcttgtg cctccgtcca tcaccatgtg ggttttgaat acctcgagc 1860  
gcctccccga tgctccgaag cctgatcttc cagggtgggg agggaaaaat cccacctccc 1920

```

ctgacctcca ccacctccac caccaccacc accaccacca ccaccactac caccaccacc 1980
caactggggc tagagtgggg aagatttccc ctttagatca aactgcccc tccatggaaa 2040
agctgaaaaa aaactctgga acccatatcc aggttgggtg aggttggctg caacagtcct 2100
ggcttcccc atccctaggc aaagagccat gagtctctga ggaggagagg accctcccca 2160
aaggactgga agcaaaaccc tctgcttctc tgggtccctc caagactccc tggggcccaa 2220
ctgtgttgct ccacctggac ccctctctcc cttctagacc tgagcttgcc cctccageta 2280
gcactaaaga acatctctgct gtaagcgctt gtaaatattc gtgaaatgtg aaacgtgcga 2340
tcttgaaact gaggtgttag aaaacttgat ctgtggtgtt ttgttttgtt ttttttctta 2400
aaacaacagc aactgaaaa aaaaaaaaaa aaa 2433

```

```

<210> 4
<211> 503
<212> PRT
<213> Homo sapiens

```

```

<400> 4
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1          5          10          15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
 20          25          30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Ser Val Ala Ala Gly
 35          40          45

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
 50          55          60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Ala Arg Glu Leu Ile Tyr
 65          70          75          80

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
 85          90          95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100          105          110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115          120          125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130          135          140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145          150          155          160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165          170          175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180          185          190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
195          200          205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln

```

210

215

220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg  
 225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu  
 245 250 255

Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys  
 260 265 270

Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu  
 275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn  
 290 295 300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser  
 305 310 315 320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly  
 325 330 335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro  
 340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu  
 355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala  
 370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala  
 385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala  
 405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn  
 420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn  
 435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu  
 450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr  
 465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala  
 485 490 495

Ser Val Gln Val Pro Arg Lys  
 500

<210> 5  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 ctgtgctgta aaaaacaagag taacattttt atattaaagt taaataaagt tacaactttg 60  
 aagagagttt ctgcaagaca tgacacaaag ctgctagcag aaaatcaaaa cgctgattaa 120  
 aagaagcacg gtatgatgac caaacataaa aagtgtttta taattgttgg tgttttaata 180  
 acaactaata ttattactct gatagttaaa ctaactcgag attctcagag ttatgcccc 240  
 tatgattgga ttggtttcca aaacaaatgc tattatttct ctaaagaaga aggagattgg 300  
 aattcaagta aatacaactg ttccactcaa catgccgacc taactataat tgacaacata 360  
 gaagaaatga attttcttag gcggtataaa tgcagttctg atcactggat tggactgaag 420  
 atggcaaaaa atcgaaacagg acaatgggta catggagcta catttacc aa atcgtttggc 480  
 atgagaggga gtgaaggatg tgccctacctc agcgatgatg gtgcagcaac agctagatgt 540  
 tacacogaaa gaaatggatg ttgcaggaaa agaatacact aagttaatgt ctaagataat 600  
 ggggaaaata gaaaataaca ttattaagtg taaaaccagc aaagtacttt tttaattaaa 660  
 caaagtctga gttttgtacc tgtctggtta attctgctta cgtgtcaggc tacacataaa 720  
 agccacttca aagattggca aaaaaaaaaa aaaaaaaaaa 759

<210> 6  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Met Thr Lys His Lys Lys Cys Phe Ile Ile Val Gly Val Leu Ile  
 1 5 10 15  
 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln  
 20 25 30  
 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr  
 35 40 45  
 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser  
 50 55 60  
 Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn  
 65 70 75 80  
 Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys  
 85 90 95  
 Met Ala Lys Asn Arg Thr Gly Gln Trp Val His Gly Ala Thr Phe Thr  
 100 105 110  
 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp  
 115 120 125  
 Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys  
 130 135 140  
 Arg Lys Arg Ile His  
 145

<210> 7  
 <211> 1086  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 ctaaagggcc cctccccgga gcggagcgca cctaggggcc ctcttcctgc cccccagccc 60  
 agctaccogt tcagaccagc agcctcgggg ggcacccccc gccagcctgc ctccctcccg 120  
 ctcagccctg ccaggggttcc ccagccatga atctctctcg attcctggga gacctctccc 180  
 acctctctgc catcatcttg ctactgctca aaatctggaa gtcccgctcg tgcgcgggaa 240  
 ttccagggaa gagccaggto ctgtttctgt tgggtgtcac tgcccgatat ctggacctct 300  
 tcaccaacta catctcactc tacaacacgt gtatgaaggt ggtctacata gcctgctcct 360  
 tcaccacggt ctggttgatt tatagcaagt tcaagctac ttacgatggg aaccatgaca 420  
 cgttcagagt ggagttcttg gtcgttccca cagccattct ggcgttcccg gtcaatcatg 480  
 acttcacccc tctggagatc ctctggacct tctccatcta cctggagatc gtggccatct 540  
 tgccgcagct gttcatgggt agcaagaccg gcgagggcga gaccatcacc agccactact 600  
 ttgtttcgct aggcgtttac cgcacgtctt atctcttcaa ctggatctgg cgctaccatt 660  
 tcgagggttt ctctgacctc atcgccattg tggcaggcct ggtccagaca gtcccttact 720  
 gcgatttctt ctacctctat atcaccaaag tcctaaaggg gaagaagttg agtttgcggg 780  
 catagccccc gtccctctcca tctctctctt cggcagcagc gggaggcaga ggaaggcggc 840  
 agaagatgaa gagctttccc atccaggggt gactttttta agaaccacc tcttgctgc 900  
 ccatcccgcc ctctctccgg gtttcagggg gacagtggag gatccaggtc ttgggggagct 960  
 caggacttgg gctgttttga gttttttgcc ttttagacaa gaaaaaaaaa tctttccact 1020  
 ctttagtttt tgattctgat gactcgtttt ttcttctact ctgtggcccc aaattttata 1080  
 aagtga 1086

<210> 8  
 <211> 212  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Asn Leu Phe Arg Phe Leu Gly Asp Leu Ser His Leu Leu Ala Ile  
 1 5 10 15  
 Ile Leu Leu Leu Leu Lys Ile Trp Lys Ser Arg Ser Cys Ala Gly Ile  
 20 25 30  
 Ser Gly Lys Ser Gln Val Leu Phe Ala Val Val Phe Thr Ala Arg Tyr  
 35 40 45  
 Leu Asp Leu Phe Thr Asn Tyr Ile Ser Leu Tyr Asn Thr Cys Met Lys  
 50 55 60  
 Val Val Tyr Ile Ala Cys Ser Phe Thr Thr Val Trp Leu Ile Tyr Ser  
 65 70 75 80  
 Lys Phe Lys Ala Thr Tyr Asp Gly Asn His Asp Thr Phe Arg Val Glu  
 85 90 95  
 Phe Leu Val Ile Pro Thr Ala Ile Leu Ala Phe Leu Val Asn His Asp  
 100 105 110  
 Phe Thr Pro Leu Glu Ile Leu Trp Thr Phe Ser Ile Tyr Leu Glu Ser  
 115 120 125



Val Ala Ile Leu Pro Gln Leu Phe Met Val Ser Lys Thr Gly Glu Ala  
 130 135 140

Glu Thr Ile Thr Ser His Tyr Leu Phe Ala Leu Gly Val Tyr Arg Thr  
 145 150 155 160

Leu Tyr Leu Phe Asn Trp Ile Trp Arg Tyr His Phe Glu Gly Phe Phe  
 165 170 175

Asp Leu Ile Ala Ile Val Ala Gly Leu Val Gln Thr Val Leu Tyr Cys  
 180 185 190

Asp Phe Phe Tyr Leu Tyr Ile Thr Lys Val Leu Lys Gly Lys Lys Leu  
 195 200 205

Ser Leu Pro Ala  
 210

<210> 9  
 <211> 3992  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60  
 ggagaagaga aggaaggaag aggaagagga agagaggaag cggagggcagg tgcggccagg 120  
 ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaaacaa gacaaacagc 180  
 cagtgccagag gagaggaacg tgtgtccagt gtcccgatcc ctgcggagct agtagctgag 240  
 agctctgtgc cctgggcacc ttgcagccct gcaactgcct gccactctcc caccgaggcc 300  
 atgggcccag gagttctgct gctcctgctg gtggccacag cttggcttgg tcagggaatc 360  
 ccagtgatag agccccagtg ccccagagctg gtctgtgaag caggagcaca ggtgaccttg 420  
 cgatgtgtgg gcaatggcag cgtggaaatgg gatggcccg catcacctca ctggaccctg 480  
 tactctgatg gctccagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540  
 acctatcgct gcaactgagcc tggagacccc ctgggaggga ggcgcgccat ccacctctat 600  
 gtcaaaagacc ctgcccggcc ctggaacgtg ctagcacagg aggtggctgt gttcgaggac 660  
 caggacgcac tactgccttg tctgtctaca gacccggtgc tggaaagcagg cgtctcgtg 720  
 gtgcgtgtgc ctgcgccggc cctcatgcgc cacaccaact actccttctc gccctggcat 780  
 ttgctcacca tccacagggc caagttcatt cagagccagg actatcaatg cagtgccctg 840  
 aggggtggca ggaaggtgat gtccatcagc atccggctga aagtgcagaa agtcatccca 900  
 gggccccagc ccttgacact ggtgcctgca gagctgtgtc ggatctcgagg ggaggctgcc 960  
 cagatcgtgt gctcagccag cagcgttgat gttaactttg atgtcttctc ccaacacaa 1020  
 aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080  
 ctgaccccca acctcgatca agtagatttc caacatccg ccaactactc ctgcgtggcc 1140  
 agcaacgtgc agggcaagca ctccacctcc atgttctctc ggggtggtaga gagtgcctac 1200  
 ttgaacttga gctctgagca gaacctcacc caggaggtga ccgtggggga ggggctcaac 1260  
 ctcaaagtca tgggtggagg ctaccacagg ctgcaagggt ttaactggag ctacctggga 1320  
 ccccttttct accaccagcc tgagcccaag ctgtctaatt ctaccacca ggacacatac 1380  
 aggcacacct tcacctcttc cttgcgccgc ctgaagccct ctgaggctcg cagctatccc 1440  
 ttcttgccca gaaacccagg aggtcgagga gctctgacgt ttgagctcac ccttgatcac 1500  
 ccccagagg taagcgtcat atggacatcc atcaacggct ctggcaccct ttgtgtgct 1560  
 gcctctgggt acccccagcc caacgtgaca tggctgcagt gcagtgggca cactgatagg 1620  
 tgtgatgagg cccaagtgtc gcaggtctgg gatgacccat accctgagg ctctgagcag 1680  
 gagccctctc caaaggtgac ggtgcagagc ctgctgactg ttgagacctt agagacacac 1740  
 caaacctcag agtgacgggc ccacaacagc gtggggagtg gctcctgggc cttcataacc 1800  
 atctctgcag gagccacac gcattccccg gatgagttcc tcttcacacc agtgggtgct 1860

accgcacgtg	ccatcatcgc	cttgcctgcgt	ctctgtgcct	gtctgctatct	gtccaagatct	1920
ccgcacatgc	ccaagtacca	ggctccgtgct	aagatcatcg	agagctatga	gggcaacagt	1980
tatacttttc	tcgacccacc	gcagctgcct	tacaacgaga	agtgggagtt	cccccggaac	2040
aaacttcgac	tttgtaagac	ctctggagct	ggagcctttg	ggaaggtgct	ggggagccagc	2100
gcctttggtc	tgggcaagca	ggatgctgtc	ctgaaggtgt	ctgtgaagat	gctgaagctg	2160
acggcccaatg	ctcatgagaa	ggaggccctc	atgtccgacg	tgaagatatt	gagccactgt	2220
ggggccacgt	agaaactctg	caacctttct	gtgcctgtga	cccatggaggt	ccctgactgc	2280
gtcatccacg	agtaactgtg	ctatggcgac	ctgtcctaact	tttgcggaag	gaaggtctgag	2340
gcgcgtgcgt	gaccacccag	gagcccccgc	caggagaccg	atggggagct	gcacataaag	2400
acaatctcac	tcgagaaaga	atatgtccgc	aggagacagc	gctctccagc	ccagggtgtg	2460
gcacacctatg	tggagatgag	gtctgtctcc	actctctcaa	atgactctct	ctcttgagca	2520
gacctggaca	aggagatggt	acggcccctg	gagctccggg	acctctgcct	ctctccagc	2580
caagtgaacc	agggcatact	cttctcctgt	tcacaagatt	gtccaccgc	gcagctggca	2640
gcgcgtaaag	tgtctgtgac	caatggctat	gtggcccaag	ttggggagct	cgggctggct	2700
aggagcatca	tgaatgaact	ccaactcaat	gtcaagggca	atgcccgct	ccctgtgaag	2760
tgtatggccc	cagagagcat	ctttgactgt	gtctcacacg	ttcagacgca	cgctctgttc	2820
ttgtgatcct	ctctctgcga	gatctctcca	cttgggctgc	atctccatcc	ttggcatctg	2880
gtgaacacga	agttctctaa	agctgtgaag	gatggatacc	aaatggccca	gcttgcattt	2940
cccccaaaac	atataataac	catcatcgag	gcctctgggt	ctcttggagc	ccccgaagca	3000
cccaactctc	agcaagatct	ctctcttctg	caggagcagc	cccaagagga	caggagagag	3060
gggctatata	ccaactctgc	gagcagcagc	agaaagcgtg	gcagccggcg	cagcacagct	3120
caggtggagg	aggagagctc	tagtgaagac	ctgacctgtg	cgcgacaaag	ggatatctgc	3180
cagcctctgc	tgcagcccac	caactatcac	ttctgtgag	gagtgacga	caggggatgc	3240
caactctccc	ttctccaaac	ttctaactct	catggatggt	ggcgacagca	gggacaacata	3300
caaaactctg	ctctggctat	ttctaactaac	agctcggccc	agctctgaaa	cttgggaagg	3360
ttagggatct	aggggagacc	agaggatacc	actctctgag	ctatgggcct	cactgcagat	3420
gcaggggtgc	gggctgagcc	ctacaccccc	gcctccccta	ctgtctctat	gggtgtggcc	3480
tcgtgttttg	ttatgccaact	gtagaacctc	tttctctcaa	ttccccttat	ttcatggaaa	3540
tggactgaact	ttatgctcat	gaagtcccca	ggagctacac	tgtagatcat	aaaacacagc	3600
ttctttgggg	tagacagacc	ggcgagagat	ggagatctcc	ttctctgagag	gacgacagca	3660
tgtcacaga	ccacactcat	ctcaggcccc	ttggagcagc	atggctcttc	taagaactct	3720
acaggacatc	ttatgcttcg	ccctatacgc	cgctctcaat	ccacagcttc	accctcccca	3780
cccccatact	ggactctgtg	tatagagcca	aggtggacat	aaaagttggg	gggtgtgtgc	3840
ccgctccgtg	catctctggc	tagaaggcag	gggacctgtg	ctatggctgt	ccacaccaag	3900
cagggaacag	aaactccccc	aagctgactc	actctaacta	acagtcaacg	cgtgggatgt	3960
ctctatccac	ataataaact	cagcattaat	gc			3992

<210> 10

<400> 10

0044007.003401

65	70	75	80
Thr Tyr Arg Cys Thr	Glu Pro Gly Asp	Pro Leu Gly Gly Ser Ala Ala	
	85	90	95
Ile His Leu Tyr Val	Lys Asp Pro Ala Arg	Pro Trp Asn Val Leu Ala	
	100	105	110
Gln Glu Val Val Val	Phe Glu Asp Gln Asp	Ala Leu Leu Pro Cys Leu	
	115	120	125
Leu Thr Asp Pro Val	Leu Glu Ala Gly Val	Ser Leu Val Arg Val Arg	
	130	135	140
Gly Arg Pro Leu Met	Arg His Thr Asn Tyr	Ser Phe Ser Pro Trp His	
	145	150	155
Gly Phe Thr Ile His	Arg Ala Lys Phe Ile	Gln Ser Gln Asp Tyr Gln	
	165	170	175
Cys Ser Ala Leu Met	Gly Gly Arg Lys Val	Met Ser Ile Ser Ile Arg	
	180	185	190
Leu Lys Val Gln Lys	Val Ile Pro Gly Pro	Pro Ala Leu Thr Leu Val	
	195	200	205
Pro Ala Glu Leu Val	Arg Ile Arg Gly Glu	Ala Ala Gln Ile Val Cys	
	210	215	220
Ser Ala Ser Ser Val	Asp Val Asn Phe Asp	Val Phe Leu Gln His Asn	
	225	230	235
Asn Thr Lys Leu Ala	Ile Pro Gln Gln Ser	Asp Phe His Asn Asn Arg	
	245	250	255
Tyr Gln Lys Val Leu	Thr Leu Asn Leu Asp	Gln Val Asp Phe Gln His	
	260	265	270
Ala Gly Asn Tyr Ser	Cys Val Ala Ser Asn	Val Gln Gly Lys His Ser	
	275	280	285
Thr Ser Met Phe Phe	Arg Val Val Glu Ser	Ala Tyr Leu Asn Leu Ser	
	290	295	300
Ser Glu Gln Asn Leu	Ile Gln Glu Val Thr	Val Gly Glu Gly Leu Asn	
	305	310	315
Leu Lys Val Met Val	Glu Ala Tyr Pro Gly	Leu Gln Gly Phe Asn Trp	
	325	330	335
Thr Tyr Leu Gly Pro	Phe Ser Asp His Gln	Pro Glu Pro Lys Leu Ala	
	340	345	350
Asn Ala Thr Thr Lys	Asp Thr Tyr Arg His	Thr Phe Thr Leu Ser Leu	
	355	360	365
Pro Arg Leu Lys Pro	Ser Glu Ala Gly Arg	Tyr Ser Phe Leu Ala Arg	

370	375	380
Asn Pro Gly Gly Trp	Arg Ala Leu Thr Phe	Glu Leu Thr Leu Arg Tyr
385	390	395
Pro Pro Glu Val Ser	Val Ile Trp Thr Phe	Ile Asn Gly Ser Gly Thr
	405	410
Leu Leu Cys Ala Ala	Ser Gly Tyr Pro Gln	Pro Asn Val Thr Trp Leu
	420	425
Gln Cys Ser Gly His	Thr Asp Arg Cys Asp	Glu Ala Gln Val Leu Gln
	435	440
Val Trp Asp Asp Pro	Tyr Pro Glu Val Leu	Ser Gln Glu Pro Phe His
	450	455
Lys Val Thr Val Gln	Ser Leu Leu Thr Val	Glu Thr Leu Glu His Asn
	465	470
Gln Thr Tyr Glu Cys	Arg Ala His Asn Ser	Val Gly Ser Gly Ser Trp
	485	490
Ala Phe Ile Pro Ile	Ser Ala Gly Ala His	Thr His Pro Pro Asp Glu
	500	505
Phe Leu Phe Thr Pro	Val Val Val Ala Cys	Met Ser Ile Met Ala Leu
	515	520
Leu Leu Leu Leu Leu	Leu Leu Leu Tyr Lys	Tyr Lys Gln Lys Pro
	530	535
Lys Tyr Gln Val Arg	Trp Lys Ile Ile Glu	Ser Tyr Glu Gly Asn Ser
	545	550
Tyr Thr Phe Ile Asp	Pro Thr Gln Leu Pro	Tyr Asn Glu Lys Trp Glu
	565	570
Phe Pro Arg Asn Asn	Leu Gln Phe Gly Lys	Thr Leu Gly Ala Gly Ala
	580	585
Phe Gly Lys Val Val	Glu Ala Thr Ala Phe	Gly Leu Gly Lys Glu Asp
	595	600
Ala Val Leu Lys Val	Ala Val Lys Met Leu	Lys Ser Thr Ala His Ala
	610	615
Asp Glu Lys Glu Ala	Leu Met Ser Glu Leu	Lys Ile Met Ser His Leu
	625	630
Gly Gln His Glu Asn	Ile Val Asn Leu Leu	Gly Ala Cys Thr His Gly
	645	650
Gly Pro Val Leu Val	Ile Thr Glu Tyr Cys	Cys Tyr Gly Asp Leu Leu
	660	665
Asn Phe Leu Arg Arg	Lys Ala Glu Ala Met	Leu Gly Pro Ser Leu Ser

675					680					685				
Pro Gly	Gln Asp	Pro Glu	Gly Gly	Val Asp	Tyr Lys	Asn Ile	His Leu							
690			695		700									
Glu Lys	Lys Tyr	Val Arg	Arg Asp	Ser Gly	Phe Ser	Ser Gln	Gly Val							
705		710		715			720							
Asp Thr	Tyr Val	Glu Met	Arg Pro	Val Ser	Thr Ser	Ser Asn	Asp Ser							
	725			730			735							
Phe Ser	Glu Gln	Asp Leu	Asp Lys	Glu Asp	Gly Arg	Pro Leu	Glu Leu							
	740			745		750								
Arg Asp	Leu Leu	His Phe	Ser Ser	Gln Val	Ala Gln	Gly Met	Ala Phe							
	755		760			765								
Leu Ala	Ser Lys	Asn Cys	Ile His	Arg Asp	Val Ala	Ala Arg	Asn Val							
	770		775			780								
Leu Leu	Thr Asn	Gly His	Val Ala	Lys Ile	Gly Asp	Phe Gly	Leu Ala							
	785		790		795		800							
Arg Asp	Ile Met	Asn Asp	Ser Asn	Tyr Ile	Val Lys	Gly Asn	Ala Arg							
		805			810		815							
Leu Pro	Val Lys	Trp Met	Ala Pro	Glu Ser	Ile Phe	Asp Cys	Val Tyr							
	820			825		830								
Thr Val	Gln Ser	Asp Val	Trp Ser	Tyr Gly	Ile Leu	Leu Trp	Glu Ile							
	835			840		845								
Phe Ser	Leu Gly	Leu Asn	Pro Tyr	Pro Gly	Ile Leu	Val Asn	Ser Lys							
	850		855		860									
Phe Tyr	Lys Leu	Val Lys	Asp Gly	Tyr Gln	Met Ala	Gln Pro	Ala Phe							
	865		870		875		880							
Ala Pro	Lys Asn	Ile Tyr	Ser Ile	Met Gln	Ala Cys	Trp Ala	Leu Glu							
		885			890		895							
Pro Thr	His Arg	Pro Thr	Phe Gln	Gln Ile	Cys Ser	Phe Leu	Gln Glu							
	900			905			910							
Gln Ala	Gln Glu	Asp Arg	Arg Glu	Arg Asp	Tyr Thr	Asn Leu	Pro Ser							
	915			920		925								
Ser Ser	Arg Ser	Gly Gly	Ser Gly	Ser Ser	Ser Ser	Glu Leu	Glu Glu							
	930		935			940								
Glu Ser	Ser Ser	Glu His	Leu Thr	Cys Cys	Glu Gln	Gly Asp	Ile Ala							
	945		950		955		960							
Gln Pro	Leu Leu	Gln Pro	Asn Asn	Tyr Gln	Phe Cys									
		965			970									

<210> 11  
 <211> 1696  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 ccgagtggtcc acacccctgtg cgtctctctg tcttgcacgc actgaggggct catccatccg 60  
 cagagcaggg cagtggggagg agacgccatg acccccattcc tccaggtctct gatctgtctc 120  
 gggctgagtc tggggcccag gacccacgtg caggcagggc accctcccaa gccaccctc 180  
 tgggctgagc caggctctgt gatcatccag ggaagtctct tgacctctag gtgtcagggg 240  
 agccttcacg agcttcagta ccactctatat agggaaaaca aatcagcattc ctgggttaga 300  
 cggatacaag agcctgggaa gaatggccag ttcccatcacc catccatcac ctgggaacac 360  
 gcagggcggt atcactgtca gtactacagc cacaaatcact catcagagta cagtgaaccc 420  
 ctggagctgg tgggtgacagg agcctacagc aaacccacccc tctcagctct gccagccct 480  
 gtggtgacct taggagggaa cgtgaccctc cagtgtgtct cacaggtggc atttgacggc 540  
 ttctattctgt gtaaggaagg agaagatgaa caccacaac gccctgaactc ccattcccat 600  
 gccctggggt ggctcctgggc catctctctc gtgggcccgc tgagcccagc tcgcaggtgg 660  
 tctgtacaggt gctatgctta tgactcgaac tctccctatg tgtgtgtctc acccagtgat 720  
 ctctctggagc tctctgtccc aggtgtttct aagaagccat cactctcagt gcagccaggt 780  
 cctatggtgg cccctgggga gagcctgacc ctccagtggt tctctgatgt cggctacgac 840  
 agatttgttc tgtataagga gggagaacgt gacttctctc agcccccctg ttggcagccc 900  
 caggctgggc tctcccagc caacttcacc ctgggcccctg tgagcccctc ccacgggggc 960  
 cagtcacagt gctacagtc acacaacctc tctctcaggt ggtgcgccc cagtgaaccc 1020  
 ctgacatcc tgcacacagg acagtcttat gacagaccct ctctctcgtt ccacggcggtc 1080  
 cccacagtag ccccaggaaa gaacgtgacc ctgctgtgtc agtcacgggg gcagttccac 1140  
 actttctctc tgaccaagga gggggcaggc catccccac tgcactcagt atcagagcac 1200  
 caagctcagc agaaccaggc tgaattccgc atgggtcctg tgacctcagc ccacgtgggg 1260  
 acctacagat gctacagctc actcagctcc aaacctacc tgcgtctctc cccagtgac 1320  
 cccctggagc tctgtgtctc agcatcccta ggccaacacc cccaggatta cacagtgagg 1380  
 aatctctacc gcatgggtgt ggctggcttg gtctctgttg tctcgggat tctcgtattt 1440  
 gaggtcagc acagccagag aagcctacaa gatgcagcgc ggaggtgaac agcagagagg 1500  
 acaatgcata ctccagcgtg gtggagcctc agggacagat ctgatgatcc caggaggctc 1560  
 tggaggacaa tctaggacct acattatctg gactgtatgc tggctcattc tagagacagc 1620  
 aatcaatatt tgagtgttaag gaaactgtct ggggtgatcc ctagaagatc attaaactgt 1680  
 ggtacatttt ttgtgc 1696

<210> 12  
 <211> 466  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly  
 1 5 10 15  
 Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp  
 20 25 30  
 Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg  
 35 40 45  
 Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn  
 50 55 60  
 Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Tyr Asn Gly  
 65 70 75 80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His  
85 90 95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu  
100 105 110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu  
115 120 125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val  
130 135 140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp  
145 150 155 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser  
165 170 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser  
180 185 190

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu  
195 200 205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro  
210 215 220

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu  
225 230 235 240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr  
245 250 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln  
260 265 270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser  
275 280 285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu  
290 295 300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe  
305 310 315 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro  
325 330 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr  
340 345 350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg  
355 360 365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro  
370 375 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser  
385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val  
405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Ser Asp Tyr Thr Val Glu Asn  
420 425 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile  
435 440 445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala  
450 455 460

Gly Arg  
465

<210> 13

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

ggcoagtgaa ttgtaatacg actcactata gggaggcggt tttttttttt tttttttttt 60  
ttt 63

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

gtcgtcaaga tgctaccgtt cagga 25

<210> 15

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

ggggacaagt ttgtacaaaa aagcaggcta tggaaaccaa cttctcca 48



```

<210> 16
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ggggaccact ttgtacaaga aagctggggtt cacattgcct gtaactcagt ctc          53

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
agcccatagc agatggcaac          20

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
tgtactttca actttgcatc ctgg          24

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
aagccaatga caaacgggat aatccctc          28

<210> 20
<211> 2051
<212> DNA
<213> Homo sapiens

<400> 20
cgccactttg ctggagcatt cactaggcga ggcgctccat cggactcact agccgcactc 60
atgaatcggc accatctgca ggatcacttt ctggaaatag acaagaagaa ctgctgtgtg 120
ttccgagatg acttcattgc caaggtgttg ccgccggtgt tggggctgga gtttatcttt 180

```

```

gggcttctggt gcaattggcct tgcctgtgtg atttctgtt tccacctcaa gtctggaaa 240
tccagccgga ttttctgtt caacctggca gtactgtact ttctactgat catctgctg 300
cggttcgtga tggactacta tgtcggcgt tcagactgga actttgggga catcccttg 360
cggctgtgtc tcttcatgtt tgccatgaac cgccaggga gcatcatctt cctcacggtg 420
gtggcggtag acaggtatctt ccgggtggct catccccacc acgcccgtgaa caagatctcc 480
aatggagacg cagccatcat ctcttgctt ctgtggggca tcactgttgg cctaacagtc 540
cacctcctga agaagaagtt gctgatccag aatggccctg caaatgtgtg catcagcttc 600
agcttcacct acatcttccg gtggcagcaa gctatgttcc tctggagatt cctctgccc 660
ctgggcatca tctgttctg ctacgcccga attatctgga gctcggcga gagacaaatg 720
gaccggcgtg ccaagatcaa gagagccatc acctcatca tgggtggggc catcgtcttt 780
gtcatctgct tcttcccag cgtggttgtg cggatccgca tcttctggct cctgcacct 840
tcggggcagc agaattgtga agtgtaccg tcggtggacc tggcgttctt tatcactctc 900
agcttcacct acatgaacag catgctggac ccggtggtgt actacttctc cagcccatcc 960
tttcccaact tcttctccac ttgatcaac cgctgcctcc agaggaagat gacaggtgag 1020
ccagataata accgcagcac gagcgtcgag ctacacgggg accccaacaa aaccagaggc 1080
gctccagagg cgtaaatggc caactccggt gagccatgga gccctcttta tctgggcccc 1140
acctcaata accattccaa gaaggacat tgcaccaaag aaccagatc tctggagaaa 1200
cagttgggtg gttgcatcga gtaattgtac tggactcggc ctaaggtttc ctggaaactc 1260
cagattcaga gaactgtatt tagggaaact gtggcagatg agtgggagac tggttgcaag 1320
gtgtgaccac aggaactcgt gaggaacaga gagtaaagct tccaggatc tgaactctg 1380
ttcatctctg acgctctcag gactgaagat gggcaaatg taggcgttt tagctgagc 1440
agttggagcc agagatctac ttgtgacttg ttggcctctt tcccactatc gctcagact 1500
ggggggggct cagctcctcg ggtgatatct agcctgctgt tagactctag caggggataag 1560
gagagctgag attggaggga attgtgttgc tctgtggaga agcccaggca tcattaaca 1620
agccagtagt tcacttgctt tccgtggacc aattcatctt tcagacaagc ttagagaaa 1680
tggactcagg gaagagactc acatgctttg gttagtatct gtgtttccgg tgggttgaat 1740
aggggattag cccagagagg gactgagcta aacagtgta ttatgggaaa ggaaatggca 1800
ttgctgcttt caaccagca ctaatgcaat coactcctct ctgttttata gtaactcaag 1860
ggttgagcag ttaaaacggc ttacagtag aaagctgttt ccacactgtt tcgttttacc 1920
attaaaaggg aaacgtgctc ctgcccacg ggtagagggg gtgcacgttc ctccgtgttc 1980
cttcgttgtt gtttctgtac ttacaaaaa tctaccactt caataaattt tgataggaga 2040
caaaaaaaaa a 2051

```

<210> 21  
 <211> 387  
 <212> PRT  
 <213> Homo sapiens

```

<400> 21
Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
 1             5             10             15

Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
 20             25             30

Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
 35             40             45

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
 50             55             60

Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
 65             70             75             80

Pro Phe Val Met Asp Tyr Trp Val Arg Arg Ser Asp Trp Asn Phe Gly
 85             90             95

```

Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln  
 100 105 110  
 Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg  
 115 120 125  
 Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala  
 130 135 140  
 Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val  
 145 150 155 160  
 His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val  
 165 170 175  
 Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met  
 180 185 190  
 Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser  
 195 200 205  
 Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala  
 210 215 220  
 Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe  
 225 230 235 240  
 Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp  
 245 250 255  
 Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val  
 260 265 270  
 Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
 275 280 285  
 Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe  
 290 295 300  
 Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu  
 305 310 315 320  
 Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn  
 325 330 335  
 Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro  
 340 345 350  
 Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys  
 355 360 365  
 Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys  
 370 375 380  
 Cys Ile Glu  
 385

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 22  
agcccatagc agatggcaac 20

<210> 23  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 23  
tgtactttca actttgcatc ctgg 24

<210> 24  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
aagccaatga caaacggat aatccctc 28